

## STIC Biotechnology Systems Branch

### RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/868,131B  
Source: 1FW/16  
Date Processed by STIC: 7/6/05

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.2.2 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):  
U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/24/05

## Raw Sequence Listing Error Summary

### ERROR DETECTED

### SUGGESTED CORRECTION

SERIAL NUMBER:

09/868,131B

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1      Wrapped Nucleics  
    Wrapped Aminos     The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2      Invalid Line Length     The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3      Misaligned Amino  
    Numbering     The numbering under each 5<sup>th</sup> amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4      Non-ASCII     The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5      Variable Length     Sequence(s)      contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6      PatentIn 2.0  
    "bug"     A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s)     . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7      Skipped Sequences  
    (OLD RULES)     Sequence(s)      missing. If intentional, please insert the following lines for each skipped sequence:  
 (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
 (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
 This sequence is intentionally skipped  
  
 Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8      Skipped Sequences  
    (NEW RULES)     Sequence(s)      missing. If intentional, please insert the following lines for each skipped sequence.  
 <210> sequence id number  
 <400> sequence id number  
 000
- 9      Use of n's or Xaa's  
    (NEW RULES)     Use of n's and/or Xaa's have been detected in the Sequence Listing.  
 Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.  
 In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10      Invalid <213>  
    Response     Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11      Use of <220>     Sequence(s)      missing the <220> "Feature" and associated numeric identifiers and responses.  
 Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.  
 (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12      PatentIn 2.0  
    "bug"     Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13      Misuse of n/Xaa     "n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid



IFW16

## RAW SEQUENCE LISTING

DATE: 07/06/2005

PATENT APPLICATION: US/09/868,131B

TIME: 12:34:17

Input Set : A:\002.00160seqlisting.txt

Output Set: N:\CRF4\07062005\I868131B.raw

3 <110> APPLICANT: Cohen, Philip  
 4 Kobayashi, Takayasu  
 5 Deak, Maria  
 7 <120> TITLE OF INVENTION: Methods Of Activating Serum Glucocorticoid Induced Protein  
 Kinase  
 9 <130> FILE REFERENCE: 002.00160  
 11 <140> CURRENT APPLICATION NUMBER: US 09/868,131B  
 12 <141> CURRENT FILING DATE: 2002-04-11  
 14 <150> PRIOR APPLICATION NUMBER: PCT/GB99/04232  
 15 <151> PRIOR FILING DATE: 1999-12-14  
 17 <150> PRIOR APPLICATION NUMBER: GB 9919676.8  
 18 <151> PRIOR FILING DATE: 1999-08-19  
 20 <150> PRIOR APPLICATION NUMBER: US 60/112,217  
 21 <151> PRIOR FILING DATE: 1998-12-14  
 23 <160> NUMBER OF SEQ ID NOS: 51  
 25 <170> SOFTWARE: PatentIn version 3.1  
 27 <210> SEQ ID NO: 1  
 28 <211> LENGTH: 367  
 29 <212> TYPE: PRT  
 30 <213> ORGANISM: Homo sapiens  
 32 <400> SEQUENCE: 1

34 Met Asn Ser Ser Pro Ala Gly Thr Pro Ser Pro Gln Pro Ser Arg Ala	
35 1 5 10 15	
38 Asn Gly Asn Ile Asn Leu Gly Pro Ser Ala Asn Pro Asn Ala Gln Pro	
39 20 25 30	
42 Thr Asp Phe Asp Phe Leu Lys Val Ile Gly Lys Gly Asn Tyr Gly Lys	
43 35 40 45	
46 Val Leu Leu Ala Lys Arg Lys Ser Asp Gly Ala Phe Tyr Ala Val Lys	
47 50 55 60	
50 Val Leu Gln Lys Lys Ser Ile Leu Lys Lys Lys Glu Gln Ser His Ile	
51 65 70 75 80	
54 Met Ala Glu Arg Ser Val Leu Leu Lys Asn Val Arg His Pro Phe Leu	
55 85 90 95	
58 Val Gly Leu Arg Tyr Ser Phe Gln Thr Pro Glu Lys Leu Tyr Phe Val	
59 100 105 110	
62 Leu Asp Tyr Val Asn Gly Gly Glu Leu Phe Phe His Leu Gln Arg Glu	
63 115 120 125	
66 Arg Arg Phe Leu Glu Pro Arg Ala Arg Phe Tyr Ala Ala Glu Val Ala	
67 130 135 140	
70 Ser Ala Ile Gly Tyr Leu His Ser Leu Asn Ile Ile Tyr Arg Asp Leu	
71 145 150 155 160	
74 Lys Pro Glu Asn Ile Leu Leu Asp Cys Gln Gly His Val Val Leu Thr	
75 165 170 175	
78 Asp Phe Gly Leu Cys Lys Glu Gly Val Glu Pro Glu Asp Thr Thr Ser	

Does Not Comply  
 Corrected Diskette Needed

pg 2, b

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TIME: 12:34:17

Input Set : A:\002.00160seqlisting.txt

Output Set: N:\CRF4\07062005\I868131B.raw

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79          180          185          190
82 Thr Phe Cys Gly Thr Pro Glu Tyr Leu Ala Pro Glu Val Leu Arg Lys
83          195          200          205
86 Glu Pro Tyr Asp Arg Ala Val Asp Trp Trp Cys Leu Gly Ala Val Leu
87          210          215          220
90 Tyr Glu Met Leu His Gly Leu Pro Pro Phe Tyr Ser Gln Asp Val Ser
91 225          230          235          240
94 Gln Met Tyr Glu Asn Ile Leu His Gln Pro Leu Gln Ile Pro Gly Gly
95          245          250          255
98 Arg Thr Val Ala Ala Cys Asp Leu Leu Gln Ser Leu Leu His Lys Asp
99          260          265          270
102 Gln Arg Gln Arg Leu Gly Ser Lys Ala Asp Phe Leu Glu Ile Lys Asn
103          275          280          285
106 His Val Phe Phe Ser Pro Ile Asn Trp Asp Asp Leu Tyr His Lys Arg
107          290          295          300
110 Leu Thr Pro Pro Phe Asn Pro Asn Val Thr Gly Pro Ala Asp Leu Lys
111 305          310          315          320
114 His Phe Asp Pro Glu Phe Thr Gln Glu Ala Val Ser Lys Ser Ile Gly
115          325          330          335
118 Cys Thr Pro Asp Thr Val Ala Ser Ser Ser Gly Ala Ser Ser Ala Phe
119          340          345          350
122 Leu Gly Phe Ser Tyr Ala Pro Glu Asp Asp Asp Ile Leu Asp Cys
123          355          360          365
126 <210> SEQ ID NO: 2
127 <211> LENGTH: 16
128 <212> TYPE: PRT
129 <213> ORGANISM: Artificial Sequence
131 <220> FEATURE:
132 <223> OTHER INFORMATION (peptide) insufficient explanation - see item 11 on
134 <400> SEQUENCE: 2 Error Summary Sheet
136 Asn Glu Glu His Asn Ser Thr Thr Ser Thr Phe Cys Gly Thr Pro Glu
137 1          5          10          15
140 <210> SEQ ID NO: 3
141 <211> LENGTH: 367
142 <212> TYPE: PRT
143 <213> ORGANISM: Mus musculus
145 <400> SEQUENCE: 3
147 Met Ala Ser Ser Pro Val Gly Val Pro Ser Pro Gln Pro Ser Arg Ala
148 1          5          10          15
151 Asn Gly Asn Ile Asn Leu Gly Pro Ser Ala Asn Pro Asn Ala Arg Pro
152          20          25          30
155 Thr Asp Phe Asp Phe Leu Lys Val Ile Gly Lys Gly Asn Tyr Gly Lys
156          35          40          45
159 Val Leu Leu Ala Lys Arg Lys Ser Asp Gly Ala Phe Tyr Ala Val Lys
160          50          55          60
163 Val Leu Gln Lys Lys Ser Ile Leu Lys Asn Lys Glu Gln Asn His Ile
164 65          70          75          80
167 Met Ala Glu Arg Asn Val Leu Leu Lys Asn Val Arg His Pro Phe Leu
168          85          90          95

```

*This error appears globally.*

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Input Set : A:\002.00160seqlisting.txt

Output Set: N:\CRF4\07062005\I868131B.raw

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171 Val Gly Leu Arg Tyr Ser Phe Gln Thr Pro Glu Lys Leu Tyr Phe Val
172      100      105      110
175 Leu Asp Tyr Val Asn Gly Gly Glu Leu Phe Phe His Leu Gln Arg Glu
176      115      120      125
179 Arg Arg Phe Leu Glu Pro Arg Ala Arg Phe Tyr Thr Ala Glu Val Ala
180      130      135      140
183 Ser Ala Ile Gly Tyr Leu His Ser Leu Asn Ile Ile Tyr Arg Asp Leu
184 145      150      155      160
187 Lys Pro Glu Asn Ile Leu Leu Asp Cys Gln Gly His Val Val Leu Thr
188      165      170      175
191 Asp Phe Gly Leu Cys Lys Glu Cys Val Glu Pro Glu Glu Thr Thr Ser
192      180      185      190
195 Thr Phe Cys Gly Thr Pro Glu Tyr Leu Ala Pro Glu Val Leu Arg Lys
196      195      200      205
199 Glu Pro Tyr Asp Arg Ala Val Asp Trp Trp Cys Leu Gly Ala Val Leu
200      210      215      220
203 Tyr Glu Met Leu His Gly Leu Pro Pro Phe Phe Asn Thr Asp Val Ala
204 225      230      235      240
207 Gln Met Tyr Glu Asn Ile Leu His Gln Pro Leu Gln Ile Pro Gly Gly
208      245      250      255
211 Arg Thr Val Ala Ala Cys Asp Leu Leu Gln Gly Leu Leu His Lys Asp
212      260      265      270
215 Gln Arg Gln Arg Leu Gly Ser Lys Glu Asp Phe Leu Asp Ile Lys Asn
216      275      280      285
219 His Met Phe Phe Ser Pro Ile Asn Trp Asp Asp Leu Tyr His Lys Arg
220      290      295      300
223 Leu Thr Pro Pro Phe Asn Pro Asn Val Glu Gly Pro Ala Asp Leu Lys
224 305      310      315      320
227 His Phe Asp Pro Glu Phe Thr Gln Glu Ala Val Ser Lys Ser Ile Gly
228      325      330      335
231 Cys Thr Pro Asp Thr Val Ala Ser Ser Ser Gly Ala Ser Ser Ala Phe
232      340      345      350
235 Leu Gly Phe Ser Tyr Ala Gln Asp Asp Asp Asp Ile Leu Asp Ser
236      355      360      365
239 <210> SEQ ID NO: 4
240 <211> LENGTH: 429
241 <212> TYPE: PRT
242 <213> ORGANISM: Homo sapiens
244 <400> SEQUENCE: 4
246 Met Ala Leu Lys Ile Pro Ala Lys Arg Ile Phe Gly Asp Asn Phe Asp
247 1      5      10      15
250 Pro Asp Phe Ile Lys Gln Arg Arg Ala Gly Leu Asn Glu Phe Ile Gln
251      20      25      30
254 Asn Leu Val Arg Tyr Pro Glu Leu Tyr Asn His Pro Asp Val Arg Ala
255      35      40      45
258 Phe Leu Gln Met Asp Ser Pro Lys His Gln Ser Asp Pro Ser Glu Asp
259      50      55      60
262 Glu Asp Glu Arg Ser Ser Gln Lys Leu His Ser Thr Ser Gln Asn Ile
263 65      70      75      80

```

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Input Set : A:\002.00160seqlisting.txt

Output Set: N:\CRF4\07062005\I868131B.raw

```

266 Asn Leu Gly Pro Ser Gly Asn Pro His Ala Lys Pro Thr Asp Phe Asp
267      85      90      95
270 Phe Leu Lys Val Ile Gly Lys Gly Ser Phe Gly Lys Val Leu Leu Ala
271      100      105      110
274 Lys Arg Lys Leu Asp Gly Lys Phe Tyr Ala Val Lys Val Leu Gln Lys
275      115      120      125
278 Lys Ile Val Leu Asn Arg Lys Glu Gln Lys His Ile Met Ala Glu Arg
279      130      135      140
282 Asn Val Leu Leu Lys Asn Val Lys His Pro Phe Leu Val Gly Leu His
283 145      150      155      160
286 Tyr Ser Phe Gln Thr Thr Glu Lys Leu Tyr Phe Val Leu Asp Phe Val
287      165      170      175
290 Asn Gly Gly Glu Leu Phe Phe His Leu Gln Arg Glu Arg Ser Phe Pro
291      180      185      190
294 Glu His Arg Ala Arg Phe Tyr Ala Ala Glu Ile Ala Ser Ala Leu Gly
295      195      200      205
298 Tyr Leu His Ser Ile Lys Ile Val Tyr Arg Asp Leu Lys Pro Glu Asn
299      210      215      220
302 Ile Leu Leu Asp Ser Val Gly His Val Val Leu Thr Asp Phe Gly Leu
303 225      230      235      240
306 Cys Lys Glu Gly Ile Ala Ile Ser Asp Thr Thr Thr Thr Phe Cys Gly
307      245      250      255
310 Thr Pro Glu Tyr Leu Ala Pro Glu Val Ile Arg Lys Gln Pro Tyr Asp
311      260      265      270
314 Asn Thr Val Asp Trp Trp Cys Leu Gly Ala Val Leu Tyr Glu Met Leu
315      275      280      285
318 Tyr Gly Leu Pro Pro Phe Tyr Cys Arg Asp Val Ala Glu Met Tyr Asp
319      290      295      300
322 Asn Ile Leu His Lys Pro Leu Ser Leu Arg Pro Gly Val Ser Leu Thr
323 305      310      315      320
326 Ala Trp Ser Ile Leu Glu Glu Leu Leu Glu Lys Asp Arg Gln Asn Arg
327      325      330      335
330 Leu Gly Ala Lys Glu Asp Phe Leu Glu Ile Gln Asn His Pro Phe Phe
331      340      345      350
334 Glu Ser Leu Ser Trp Ala Asp Leu Val Gln Lys Lys Ile Pro Pro Pro
335      355      360      365
338 Phe Asn Pro Asn Val Ala Gly Pro Asp Asp Ile Arg Asn Phe Asp Thr
339      370      375      380
342 Ala Phe Thr Glu Glu Thr Val Pro Tyr Ser Val Cys Val Ser Ser Asp
343 385      390      395      400
346 Tyr Ser Ile Val Asn Ala Ser Val Leu Glu Ala Asp Asp Ala Phe Val
347      405      410      415
350 Gly Phe Ser Tyr Ala Pro Pro Ser Glu Asp Leu Phe Leu
351      420      425
354 <210> SEQ ID NO: 5
355 <211> LENGTH: 2146
356 <212> TYPE: DNA
357 <213> ORGANISM: Homo sapiens
359 <400> SEQUENCE: 5

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Input Set : A:\002.00160seqlisting.txt

Output Set: N:\CRF4\07062005\I868131B.raw

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360 atggggttcag actttatgcc ctgaaaagat ccttcacgcc ctggccatct tggacttctg      60
362 gagctaccct ggctcacagg ggtcttggtg ccttgggtgt cccagttct tgaaaagaat      120
364 cagcctggga ggggccacac cctgaccatc cccctttatc cttcttgaga tgtttgttag      180
366 gaagtctggg tccaggggat atcatttctt gttccatcca tgcaggggtt gcttacctcg      240
368 ggtaggaaac cctcaggcgg tggcaggtgc acaggtaggg gaggatggag agggcagtg      300
370 tgcctgaagc cctggatggg cggagctgac ccccaacac caactctatc atgcctgctc      360
372 ctccctgtcc cccagagct gcctgatcat tgctacagaa tgaactctag cccagctggg      420
374 accccaagtc cacagccctc cagggccaat gggaacatca acctggggcc ttcagccaac      480
376 ccaaagtcac agcccacgga cttcgacttc ctcaaagtca tgggcaaagg gaactacggg      540
378 aaggctctac tggccaagcg caagtctgat ggggcgttct atgcagtga ggtactacag      600
380 aaaaagtcca tcttaaagaa gaaagagcag agccacatca tggcagagcg cagtgtgctt      660
382 ctgaagaacg tgcggcacc cttcctcgtg ggctgcgct actccttcca gacacctgag      720
384 aagctctact tcgtgctcga ctatgtcaac gggggagagc tcttcttcca cctgcagcgg      780
386 gagcgccggg tccctggagc cggggccagg ttctacgctg ctgaggtggc cagcgccatt      840
388 ggctacctgc actccctcaa catcatttac agggatctga aaccagagaa cattctcttg      900
390 gactgccagg gacacgtggt gctgacggat tttggcctct gcaaggaagg tgtagagcct      960
392 gaagacacca catccacatt ctgtggtacc cctgagtact tggcacctga agtgcttcgg      1020
394 aaagagcctt atgatcgagc agtggactgg tgggtgcttg gggcagtcct ctacgagatg      1080
396 ctccatggcc tgcgcctt ctacagccaa gatgtatccc agatgtatga gaacattctg      1140
398 caccagccgc tacagatccc cggaggccgg acagtggccg cctgtgacct cctgcaaagc      1200
400 cttctccaca aggaccagag gcagcggctg ggctccaaag cagactttct tgagattaag      1260
402 aacctgtat tcttcagccc cataaactgg gatgacctgt accacaagag gctaactcca      1320
404 cccttcaacc caaatgtgac aggacctgct gacttgaagc attttgacct agagttcacc      1380
406 caggaagctg tgtccaagtc cattggctgt acccctgaca ctgtggccag cagctctggg      1440
408 gcctcaagtg cattcctggg attttcttat gcgccagagg atgatgacat cttggattgc      1500
410 tagaagagaa ggacctgtga aactactgag gccagctggt attagtaagg aattaccttc      1560
412 agctgctagg aagagcgact caaactaaca atggcttcaa cgagaagcag gtttattttt      1620
414 tccagcacat aaaagaaaaa taatgtttcg gagtccagga ctggcaggac aggtcatcag      1680
416 atactcagag gctgtatctc tgccctgcca accttgacaa atggcttcca atgttaggtt      1740
418 tgctacaaga tggttactgg agctctagct gcctattttg tgtttagggg agggaaaatg      1800
420 gaggaaggag gagaagagca aaggcgctt ttaaagagct tcccaaaag ccccccaa      1860
422 tgacttttgc ttccatctca ctaaccaccc acccctacct ggaatggagg ctgggaaatg      1920
424 tggcttattt gctgggtacg tgactatccc taataacaaa ggggttttga ccctaagaca      1980
426 ttaggggaga atgttgggta ggcagccagc cctcttttac catagggcct cctggtgttt      2040
428 ggattttgat ctcaatgtgt aaaatgacag agatgtaaca agctcatagg gtatcaatat      2100
430 ctcttattgt tctatgttga aaaaaaaaaa aaaaaaaaaa aaaaaa      2146
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434 <211> LENGTH: 2404
435 <212> TYPE: DNA
436 <213> ORGANISM: Homo sapiens
438 <400> SEQUENCE: 6
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443 tataaagttc tggtttcagt gggagaagat gaatggtttg tcttcaggag atatgcagag      180
445 tttgataaac tttataacac tttaaaaaaa cagtttctct ctatggccct gaagattcct      240
447 gccaaagagaa tatttgggtga taattttgat ccagatttta ttaaacaaag acgagcagga      300
449 ctaaacgaat tcattcagaa cctagttagg tatccagaac tttataacca tccagatgtc      360
451 agagcattcc ttcaaatgga cagtcacaaa caccagtcag atccatctga agataggat      420
453 gaaagaagtt ctcagaagct acactctacc tcacagaaca tcaacctggg accgtctgga      480

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RAW SEQUENCE LISTING ERROR SUMMARY  
PATENT APPLICATION: US/09/868,131B

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TIME: 12:34:18

Input Set : A:\002.00160seqlisting.txt  
Output Set: N:\CRF4\07062005\I868131B.raw

*FYI*  
Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:45; Xaa Pos. 2,3,4,5,6  
Seq#:46; Xaa Pos. 2,4,5,6  
Seq#:47; Xaa Pos. 2,4,5,6,7  
Seq#:48; Xaa Pos. 1,7,8,10  
Seq#:49; Xaa Pos. 1,2,3,4,5,6,7



**VERIFICATION SUMMARY**

DATE: 07/06/2005

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TIME: 12:34:18

Input Set : A:\002.00160seqlisting.txt

Output Set: N:\CRF4\07062005\I868131B.raw

L:1204 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:45 after pos.:0  
L:1236 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:46 after pos.:0  
L:1274 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:47 after pos.:0  
L:1312 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:48 after pos.:0  
L:1362 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:49 after pos.:0